

1646

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/816,011C

DATE: 02/14/2001
TIME: 17:54:56

Input Set : A:\11420121.app
Output Set: N:\CRF3\02142001\H816011C.raw

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f.s MAR 01 2001

TECH CENTER 1600/2900

3 <110> APPLICANT: Pausch, Mark H
 4 Price, Laura A
 6 <120> TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
 7 AND METHODS OF USING SAME
 9 <130> FILE REFERENCE: 01142.0122 SEQUENCE LISTING
 11 <140> CURRENT APPLICATION NUMBER: 08/816,011C
 12 <141> CURRENT FILING DATE: 1997-03-11
 14 <150> PRIOR APPLICATION NUMBER: 08/332,312
 15 <151> PRIOR FILING DATE: 1994-10-31
 17 <150> PRIOR APPLICATION NUMBER: PCT/US95/14364
 18 <151> PRIOR FILING DATE: 1995-10-25
 20 <160> NUMBER OF SEQ ID NOS: 64
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 2441
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Drosophila melanogaster
 29 <400> SEQUENCE: 1
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 31 cttaaaaaga aaaaaaaaaat aataagtcaa aactacaaac cacacagcg aaggcgaaag 120
 32 caacggttcc tgcgagtgta tattttttt ttcaacaatt ttgatcgta gtgcgacaat 180
 33 ccgtcgagca tgtcgcccga tcgatggatc ctgctgctca tcttctacat atcctacctg 240
 34 atgttcgggg cggcaatcta ttaccatatt gacacggcg aggagaagat atcgcgcgccc 300
 35 gaacagcgca aggcgcaaat tgcaatcaac gaatatctgc tggaggagct gggcgacaag 360
 36 aatacgacca cacaggatga gattctcaa cgatctcg attactgtga caaaccgggtt 420
 37 acatgccgc cgacatatacg tgatacgccc tacacgtgga ccttctacca tgccttc 480
 38 ttgccttca cgggttgcac cgggtggga tatgggaata tgcgccaac caccctcgcc 540
 39 ggacggatcg tcatgatcgat gtattcggtt atggcatcc cggtaatgg tatctctttt 600
 40 gcccgcctcg gcaatactt tgjacgtacg ttgaaagcgatc tctacagacg ctacaaaaag 660
 41 tacaagatgt ccacggatata gcaactatgtc cccggcgcage tgggattgtt caccacgggt 720
 42 gtgattgccc tgattccggg aatagtc ttcctgggtc tgccctgcgt ggggttccac 780
 43 ctacttcgag aactggccatcttccatc tgcgtgtact acagctatgt gaccaccaca 840
 44 acaattggat tgggtgacta tggccaca ttggagcca accagccaa ggagttccgc 900
 45 ggctggttcg tggcttatca gatctttgtt atcgatgtt tcatcttc gctggatata 960
 46 cttgtatga tcatgacatt tatcactcg ggcctccaga gcaagaagct ggcatacctg 1020
 47 gagcagcgt tgcctccaa cctgaaggcc acacagaatc gcatctgtc tggcgtcacc 1080
 48 aaggatgtgg gtcaccccg gcaatgtc aacgagctgt acatcccaa agtgaagcct 1140
 49 gtgtacaccg atgttagatata cgccatcacaca ctgccccgtt ccaattcgatc tccgatctg 1200
 50 agcatgttacc gcgtggagcc ggctccatt cccagccgg aaggggcatc ctccgtgtc 1260
 51 gcccacatgg ttggcgccca aaggaggcg ggcattgtac acgcaatcc cgatacggat 1320
 52 ctaaccaaac tggatcgatcgaa gagacatcc gagacggcg aggcttacca ccagaccacc 1380
 53 gatttgcgtt ccaagggtggt caacgcactg gccacgggtg agccaccggc ggcggAACAG 1440
 54 gaagatgcgg ctctctatgg tggcttatcat ggcttctccg actcccgat cctggccagc 1500
 55 gaatggtcgt ttcgcacggt caacgagttt acatcaccgc gacgttcaag agcacgtgcc 1560
 56 tgctccgatt tcaatctggaa ggcaccccg tggcagagcg agaggccact gcttgcgagc 1620
 57 cacaacgaat ggacatggag cggcgacaac cagcagatcc aggaggcatt caaccagcgc 1680
 58 tacaaggac agcagcgtgc caacggagca gccaactcgatccatggtcca tctggagccg 1740

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59 gatgctttgg aggagcagct gagaacaat caccgggtgc cggtcgctc aagaagtct 1800
 60 ccatgccgga tggtctcgca cgtctgttc cttccagaa gaagcacccc tcgcaggatc 1860
 61 tggagcgcaa gttgtccgtg gtctcggtac ccgagggtgt catctcgag gaagccagat 1920
 62 ccccgctgga ctactacatc aacacggtaa cgccggcctc cagtcaatcc tatttgcga 1980
 63 acggacgcgg tccgccccccg cccttcaat cgaatggcag cttggccacg ggcggccggcg 2040
 64 ggctaacgaa catggcgttc cagatggagg atggagcaac cccggccatcg gcatatggcg 2100
 65 gtggaggccta tcaacgcaag ggggtcgctg gcaagcgccg acgcgagagc atctacaccc 2160
 66 agaatcaagc cccatccgtc cgccggggca gcatgtatcc ggcgaccccg cacgccttgg 2220
 67 cccagatgca gatgcgacgc ggcaggttg caaccatggg ctctggatcg ggcggccatgg 2280
 68 cggcgtggc cgccgtcggt ggcaggtcttccaggtac agcatggca tcatcgctga 2340
 69 cctctgtcc ggcggaaagc agcatattct cggttaccccgaaaaggat atgaatgtgc 2400
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 74 <211> LENGTH: 618
 75 <212> TYPE: PRT
 76 <213> ORGANISM: Drosophila melanogaster
 78 <400> SEQUENCE: 2
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 80 1 5 10 15
 82 Leu Met Phe Gly Ala Ala Ile Tyr Tyr His Ile Glu His Gly Glu Glu
 83 20 25 30
 85 Lys Ile Ser Arg Ala Glu Gln Arg Lys Ala Gln Ile Ala Ile Asn Glu
 86 35 40 45
 88 Tyr Leu Leu Glu Glu Leu Gly Asp Lys Asn Thr Thr Thr Gln Asp Glu
 89 50 55 60
 91 Ile Leu Gln Arg Ile Ser Asp Tyr Cys Asp Lys Pro Val Thr Leu Pro
 92 65 70 75 80
 94 Pro Thr Tyr Asp Asp Thr Pro Tyr Thr Trp Thr Phe Tyr His Ala Phe
 95 85 90 95
 97 Phe Phe Ala Phe Thr Val Cys Ser Thr Val Gly Tyr Gly Asn Ile Ser
 98 100 105 110
 100 Pro Thr Thr Phe Ala Gly Arg Met Ile Met Ile Ala Tyr Ser Val Ile
 101 115 120 125
 103 Gly Ile Pro Val Asn Gly Ile Leu Phe Ala Gly Leu Gly Glu Tyr Phe
 104 130 135 140
 106 Gly Arg Thr Phe Glu Ala Ile Tyr Arg Arg Tyr Lys Lys Tyr Lys Met
 107 145 150 155 160
 109 Ser Thr Asp Met His Tyr Val Pro Pro Gln Leu Gly Leu Ile Thr Thr
 110 165 170 175
 112 Val Val Ile Ala Leu Ile Pro Gly Ile Ala Leu Phe Leu Val Leu Pro
 113 180 185 190
 115 Cys Val Gly Val His Leu Leu Arg Glu Leu Gly Leu Ser Ser Ile Ser
 116 195 200 205
 118 Leu Tyr Tyr Ser Tyr Val Thr Thr Thr Ile Gly Phe Gly Asp Tyr
 119 210 215 220
 121 Val Pro Thr Phe Gly Ala Asn Gln Pro Lys Glu Phe Gly Gly Trp Phe
 122 225 230 235 240
 124 Val Val Tyr Gln Ile Phe Val Ile Val Trp Phe Ile Phe Ser Leu Gly
 125 245 250 255

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127 Tyr Leu Val Met Ile Met Thr Phe Ile Thr Arg Gly Leu Gln Ser Lys
128 260 265 270
130 Lys Leu Ala Tyr Leu Glu Gln Gln Leu Ser Ser Asn Leu Lys Ala Thr
131 275 280 285
133 Gln Asn Arg Ile Trp Ser Gly Val Thr Lys Asp Val Gly Tyr Leu Arg
134 290 295 300
136 Arg Met Leu Asn Glu Leu Tyr Ile Leu Lys Val Lys Pro Val Tyr Thr
137 305 310 315 320
139 Asp Val Asp Ile Ala Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp
140 325 330 335
142 Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ile Pro Ser Arg Lys Arg
143 340 345 350
145 Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly
146 355 360 365
148 Met Val His Ala Asn Ser Asp Thr Asp Leu Thr Lys Leu Asp Arg Glu
149 370 375 380
151 Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu
152 385 390 395 400
154 Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Pro Ala Glu
155 405 410 415
157 Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe Ser Asp Ser
158 420 425 430
160 Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr
161 435 440 445
163 Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu
164 450 455 460
166 Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu
167 465 470 475 480
169 Trp Thr Trp Ser Gly Asp Asn Gln Gln Ile Gln Glu Ala Phe Asn Gln
170 485 490 495
172 Arg Tyr Lys Gly Gln Gln Arg Ala Asn Gly Ala Ala Asn Ser Thr Met
173 500 505 510
175 Val His Leu Glu Pro Asp Ala Leu Glu Glu Gln Leu Arg Asn Asn His
176 515 520 525
178 Arg Val Pro Val Ala Ser Arg Ser Ser Pro Cys Arg Met Val Cys Asp
179 530 535 540
181 Val Cys Phe Pro Ser Arg Arg Ser Thr Pro Arg Arg Ile Trp Ser Ala
182 545 550 555 560
184 Ser Cys Pro Trp Ser Arg Tyr Pro Arg Val Ser Ser Arg Arg Lys Pro
185 565 570 575
187 Asp Pro Arg Trp Thr Thr Ser Thr Arg Ser Arg Arg Pro Pro Val
188 580 585 590
190 Asn Pro Ile Cys Ala Thr Asp Ala Val Arg His Arg Pro Ser Asn Arg
191 595 600 605
193 Met Ala Ala Trp Pro Ala Ala Ala Gly
194 610 615
197 <210> SEQ ID NO: 3
198 <211> LENGTH: 1011
199 <212> TYPE: DNA

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200 <213> ORGANISM: Caenorhabditis elegans
 202 <400> SEQUENCE: 3
 203 atgtccgatc agctgttgt cgcatggag aagtatttct tgacgagtaa cgaggtaag 60
 204 aagaatgcag caacggagac atggacattt tcatcgcca ttttcttgc cgtaaccgtc 120
 205 gtcactacca tcggatacgg taatccagtt ccagtgcaca acattggacg gatatgggt 180
 206 atattgttct ccttgcttg aatacctcta acactggta ccatcgctga ctggcagg 240
 207 aaattccat ctgaacatct tggttgggt tatggaaact atttggaaatt aaaatatctc 300
 208 atattgtcac gacatcgaaa agaacggaga gggcacgtt gtgagcactg tcacagtcat 360
 209 ggaatggggc atgatggaa tatcgaggag aaaagaattt ctgcattctt ggtttagt 420
 210 attctgtatg tatatacagc gtttgcgtt gtcctaattgt caaaatttga gccgtggct 480
 211 ttcttcattt cattctactg gtccttcattt acaatgacta ctgtcggtt tggcgactt 540
 212 atgcccagaa gggacggata catgtatatac atattgtctt atatcattttt aggtaaattt 600
 213 tcaatgaaaa aaaaacaaaa attcaaaaata tttttagtgc ttgcaataac tacaatgtc 660
 214 attgatttgg taggagtaca gtatattcga aagatttattt atttcgaaag aaaaatttcaa 720
 215 gacgctagat ctgcatttgc gttttagga ggaaaggtag tccttgatc agaactctac 780
 216 gcaaaatttta tgcaaaagcg agctcgtaac atgtccccgag aagcttttat agtggagaat 840
 217 ctctatgttt ccaaaccat cataccattt ataccaactg atatccgatg tattcgat 900
 218 attgatcaaa ctgccatgc tgctaccatt tccacgtcat cgtctgcaat tgatatgcaa 960
 219 agttgtatg tttgttatttctt aagatattctt ctcaatcgat cattcaataa g 1011
 222 <210> SEQ ID NO: 4
 223 <211> LENGTH: 336
 224 <212> TYPE: PRT
 225 <213> ORGANISM: Drosophila melanogaster
 227 <400> SEQUENCE: 4
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 229 1 5 10 15
 231 Asn Glu Val Lys Lys Asn Ala Ala Thr Glu Thr Trp Thr Phe Ser Ser
 232 20 25 30
 234 Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn
 235 35 40 45
 237 Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser
 238 50 55 60
 240 Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Asp Leu Ala Gly
 241 65 70 75 80
 243 Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys
 244 85 90 95
 246 Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His
 247 100 105 110
 249 Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile
 250 115 120 125
 252 Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val
 253 130 135 140
 255 Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser
 256 145 150 155 160
 258 Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly
 259 165 170 175
 261 Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu
 262 180 185 190
 264 Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Gln Lys Phe

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265      195          200          205
267 Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val
268      210          215          220
270 Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln
271      225          230          235          240
273 Asp Ala Arg Ser Ala Leu Ala Val Val Gly Gly Lys Val Val Leu Val
274      245          250          255
276 Ser Glu Leu Tyr Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser
277      260          265          270
279 Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile
280      275          280          285
282 Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr
283      290          295          300
285 Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ala Ile Asp Met Gln
286 305      310          315          320
288 Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys
289      325          330          335
295 <210> SEQ ID NO: 5
296 <211> LENGTH: 51
297 <212> TYPE: DNA
298 <213> ORGANISM: Caenorhabditis elegans
300 <400> SEQUENCE: 5
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304 <210> SEQ ID NO: 6
305 <211> LENGTH: 51
306 <212> TYPE: DNA
307 <213> ORGANISM: Caenorhabditis elegans
309 <400> SEQUENCE: 6
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314 <211> LENGTH: 24
315 <212> TYPE: PRT
316 <213> ORGANISM: Drosophila melanogaster
318 <400> SEQUENCE: 7
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322 Arg Cys Val Thr Asp Glu Cys Pro
323      20
326 <210> SEQ ID NO: 8
327 <211> LENGTH: 24
328 <212> TYPE: PRT
329 <213> ORGANISM: Drosophila melanogaster
331 <400> SEQUENCE: 8
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333      1           5           10          15
335 Arg Cys Val Thr Glu Gln Cys Ala
336      20
339 <210> SEQ ID NO: 9
340 <211> LENGTH: 24

```

FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/08/816,011C

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Input Set : A:\11420121.app
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L:859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:1035 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1069 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1070 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:1189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:1195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:1226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:1346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
L:1367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
L:1409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
L:1430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
L:1463 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60
L:1493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
L:1690 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64